

SEQUENCE LISTING

<110> Cla Emond, Stephanie K.
Sensibar, Debra K.

<120> CTR1 HOMOLOGUE FROM MELON

<130> 4257-01/24.30

<140> Not Yet Assigned

<141> Filed Herewith

<150> US 60/218,307

<151> 2000-07-14

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3236

<212> DNA

<213> Cucumis melo

<220>

<221> misc_feature

<222> (31)...(51)

<223> n = A,T,C or G

<220>

<221> misc_feature

<222> (503)...(544)

<223> n = A,T,C or G

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- <210> 2
- <211> 250
- <212> FRT
- <213> Cucumis melo

<220>
<221> VARIANT
<222> (154)... (154)
<223> Xaa = Any Amino Acid

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20 25 30
Val Ala Ala Gly Gly Asn Val Ile Lys Gly Arg Thr Asp Arg Val Phe
35 40 45
Asp Trp Asp Gly Ser Gly Asp His Asn Leu Asn Thr Gln Ala Tyr Arg
50 55 60
Ile Gly Asn Leu Tyr Ser Trp Ile Gly Leu Gln Arg His Ser Ser Gly
65 70 75 80
Ser Ser Tyr Asp Asp Ser Ser Leu Ser Ser Asp Tyr Tyr Ala Pro Thr
85 90 95
Leu Ser Asn Pro Ala Ala Asn Glu Ile Asn Ala Leu Glu Tyr Ile Leu
100 105 110
Asp Asp Asp Phe Arg Val Met Lys Ala Val Gly Ser Gly Gly Ser Ser
115 120 125
Gly Lys Ser Trp Ala Gln Gln Thr Glu Ala Ser Phe Gln Leu Gln Gln
130 135 140
Pro Leu Val Leu Arg Leu Ser Ser Asp Asn Phe Cys Ala Asp Asp Pro
145 150 155 160

Asn Phe Met Asp Ile Ile Pro Asp Glu Ala Arg Ile Arg Ser Leu Ser
 175
 Ile Ser Ala Glu Ala Ile Ser His Arg Phe Ile Val Asn Gly Cys Met
 180 185 190
 Ser Tyr Leu Glu Lys Val Pro Asp Gly Phe Tyr Leu Ile His Gly Met
 195 200 205
 Asp Pro Tyr Val Trp Ser Leu Cys Thr Asn Leu Glu Glu Asp Gly Arg
 210 215 220
 Ile Pro Ser Phe Glu Ser Leu Lys Thr Val Asp Ser Ser Ile Gly Ser
 225 230 235 240
 Ser Ile Glu Val Val Leu Ile Asp Arg His Ser Asp Ala Ser Leu Lys
 245 250 255
 Glu Leu Gln Asn Arg Val His Asn Ile Ser Ser Ser Cys Val Thr Thr
 260 265 270
 Lys Glu Val Ala Asp His Ile Ala Lys Leu Val Cys Asn His Leu Gly
 275 280 285
 Gly Ser Val Ser Glu Gly Glu Asp Asp Leu Val Ser Ala Trp Lys Glu
 290 295 300
 Cys Ser Asp Asp Leu Lys Glu Cys Leu Gly Ser Ala Val Ile Pro Leu
 305 310 315 320
 Cys Ser Leu Ser Val Gly Leu Cys Arg His Arg Ala Leu Leu Phe Lys
 325 330 335
 Val Leu Ala Asp Ser Ile Asp Leu Pro Cys Arg Ile Ala Lys Gly Cys
 340 345 350
 Lys Tyr Cys Thr Arg Asp Asp Ala Ser Ser Cys Leu Val Arg Phe Gly
 355 360 365
 Leu Asp Arg Glu Tyr Leu Ile Asp Leu Ile Gly Arg Pro Gly Cys Leu
 370 375 380
 Cys Gln Pro Asp Ser Leu Leu Asn Gly Pro Ser Ser Ile Ser Ile Ser
 385 390 395 400
 Ser Pro Leu Arg Phe Pro Arg Leu Lys Pro Ile Glu Ser Thr Ile Asp
 405 410 415
 Phe Arg Ser Leu Ala Lys Gln Tyr Phe Leu Asp Ser Gln Ser Leu Asn
 420 425 430
 Leu Val Phe Asp Glu Ala Ser Ser Gly Asp Val Val Ser Gly Lys Asp
 435 440 445
 Ala Ala Phe Ser Val Tyr Gln Arg Pro Leu Asn Arg Lys Asp Val Asp
 450 455 460
 Gly Lys Thr Ile Val Val Thr Gly Asp Lys Asp Arg Asn Ser Gln Leu
 465 470 475 480
 Leu Asn Lys Lys Ala Ala Gln Leu Asn Thr Gln Asp Gly Lys Ser Glu
 485 490 495
 Gln Phe Arg Ser Cys Val Ala Ser Pro Tyr Ser Val Gln Ser Thr Pro
 500 505 510
 Phe Val Glu Asn Val Val Pro Leu Ser His Ile Ser His Ile Gly Ser
 515 520 525
 Glu Asp Ser Glu His Leu Leu Ala Leu Ser His Pro Arg Met Asp His
 530 535 540
 Val Asn Asn Leu Pro Phe Val His Gly Ser Ser Leu Ile Arg Lys Pro
 545 550 555 560
 Asn Glu Leu Ser Leu Gly Leu Glu Asp Leu Tyr Ile Pro Trp Thr Asp
 565 570 575
 Leu Asp Leu Arg Glu Lys Ile Gly Ala Gly Ser Phe Gly Thr Val Tyr
 580 585 590
 Arg Gly Glu Trp His Gly Ser Asp Val Ala Val Lys Ile Leu Thr Glu
 595 600 605
 Gln Asp Phe His Pro Glu Arg Val Asn Glu Tyr Leu Arg Glu Val Ala
 610 615 620
 Ile Met Lys Ser Leu Arg His Pro Asn Ile Leu Phe Met Gly Ala
 625 630 635 640
 Val Thr Lys Pro Pro Asn Leu Ser Ile Val Tyr Glu Tyr Leu Ser Arg
 645 650 655

Gly Ser Leu Tyr Arg Leu Leu His Lys Ser Val Val Lys Asp Ile Asp
 660 665 670
 Gly Thr Arg Arg Ile Asn Met Ala Phe Asp Val Val Lys Gly Met Asn
 675 680 685
 Tyr Leu His Arg Arg Asp Pro Pro Ile Val His Arg Asp Leu Lys Ser
 690 695
 Pro Asn Leu Leu Val Asp Lys Lys Tyr Thr Val Tyr Val Cys Asp Phe
 700 710 715 720
 Gly Leu Ser Arg Leu Lys Ala Arg Thr Phe Leu Ser Ser Lys Ser Ala
 725 730 735
 Ala Gly Thr Pro Glu Trp Met Ala Pro Glu Val Leu Arg Asp Glu Pro
 740 745 750
 Ser Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu
 755 760 765
 Leu Ala Thr Leu Gln Gln Pro Trp Cys Asn Leu Asn Pro Ala Gln Val
 770 775 780
 Val Ala Ala Val Gly Phe Lys Gly Lys Arg Leu Asp Ile Pro Arg Asp
 785 790 795 800
 Val Asn Pro Lys Leu Ala Ser Leu Ile Val Ala Cys Trp Ala Asp Glu
 805 810 815
 Pro Trp Lys Arg Pro Ser Phe Ser Ser Ile Met Glu Thr Leu Lys Pro
 820 825 830
 Met Thr Lys Gln Ala Pro Pro Gln Gln Ser Arg Thr Asp Thr Leu Ser
 835 840 845
 Val Met
 850

<210> 3
 <211> 28
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 <213> sArtificial Sequence

<220>
 <221> synthetic oligonucleotide

<400> 3
 caatatttac atccyttggc aattcgac

28

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> synthetic oligonucleotide

<400> 4
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29

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> synthetic oligonucleotide

<400> 5
 atgtttggga totgttgga ttcc

24

<210> 6
 <211> 24

<210> DNA
<213> Artificial Sequence

<210>
<213> synthetic oligonucleotide

<400> 6
ttt gtt ggt tgg tca aag aac

24

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<210>
<213> synthetic oligonucleotide

<400> 7
cct ggt tgc ttctccat at agt

24

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<210>
<213> synthetic oligonucleotide

<400> 8
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24